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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/377,675

DATE: 09/02/1999  
TIME: 11:06:35

Input Set: I377675.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: Olwin, Bradley B.
2 Rosenthal, Richard S.
3 <120> TITLE OF INVENTION: CHIMERIC FIBROBLAST GROWTH FACTOR PROTEINS, NUCLEIC
4 ACID MOLECULES, AND USES THEREOF
5 <130> FILE REFERENCE: 2848-32
6 <140> CURRENT APPLICATION NUMBER: US/09/377,675
7 <141> CURRENT FILING DATE: 1999-08-19
8 <150> EARLIER APPLICATION NUMBER: 60/097,160
9 <151> EARLIER FILING DATE: 1998-08-19
10 <160> NUMBER OF SEQ ID NOS: 27
11 <170> SOFTWARE: PatentIn Ver. 2.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 556
14 <212> TYPE: DNA
15 <213> ORGANISM: chimeric sequence
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (8)..(553)
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21 Met Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys
22 1 5 10
23 tgg aaa aag gcg gct gct ggt tct atc act acc ctg cca gct ctg cca 97
24 Trp Lys Lys Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro
25 15 20 25 30
26 gaa gac ggt ggt tct ggt gcc ttc cca cca ggt cac ttc aaa gac cca 145
27 Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro
28 35 40 45
29 aaa cgt ctg tac tgc aaa aac ggt ggt ttc ttc ctg cgc atc cac ccc 193
30 Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro
31 50 55 60
32 gac ggc cga gtg gac ggg gtc cgc gag aag agc gac cca cac atc aaa 241
33 Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys
34 65 70 75
35 cta caa ctt caa gca gaa gag aga ggg gtt gtg tct atc aaa gga gtg 289
36 Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val
37 80 85 90
38 tgt gca aac cgt tac ctt gct atg aaa gaa gat gga aga tta cta gct 337
39 Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala
40 95 100 105 110
41 tct aaa tgt gtt aca gac gag tgt ttc ttt ttt gaa cga ttg gag tct 385
42 Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser
43 115 120 125
44 aat aac tac aat act tac cgg tca agg aaa tac acc agt tgg tat gtg 433

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45      Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val
46              130              135              140
47      gca ctg aaa cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct      481
48      Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro
49              145              150              155
50      ggg cag aaa gct ata ctt ttt ctt cca atg tct gct aag agc gaa cag      529
51      Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln
52              160              165              170
53      aaa ctc atc tct gaa gag gat ctg tga      556
54      Lys Leu Ile Ser Glu Glu Asp Leu
55      175              180
56 <210> SEQ ID NO 2
57 <211> LENGTH: 182
58 <212> TYPE: PRT
59 <213> ORGANISM: chimeric sequence
60 <400> SEQUENCE: 2
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62              1              5              10              15
63      Lys Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp
64              20              25              30
65      Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg
66              35              40              45
67      Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly
68              50              55              60
69      Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln
70              65              70              75              80
71      Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala
72              85              90              95
73      Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys
74              100              105              110
75      Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn
76              115              120              125
77      Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu
78              130              135              140
79      Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln
80              145              150              155              160
81      Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln Lys Leu
82              165              170              175
83      Ile Ser Glu Glu Asp Leu
84              180
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86 <211> LENGTH: 556
87 <212> TYPE: DNA
88 <213> ORGANISM: chimeric sequence
89 <220> FEATURE:
90 <221> NAME/KEY: CDS
91 <222> LOCATION: (11)..(553)
92 <400> SEQUENCE: 3
93      ggtagtccat atg ggc cgc aaa aaa cgc cgc cag cgc cgc cgc ccg ccg      49
94      Met Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro

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95          1          5          10
96  cag gaa ttc gcg gct gct ggt tct atc act acc ctg cca gct ctg cca 97
97  Gln Glu Phe Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro
98          15          20          25
99  gaa gac ggt ggt tct ggt gcc ttc cca cca ggt cac ttc aaa gac cca 145
100 Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro
101          30          35          40          45
102  aaa cgt ctg tac tgc aaa aac ggt ggt ttc ttc ctg cgc atc cac ccc 193
103  Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Leu Arg Ile His Pro
104          50          55          60
105  gac ggc cga gtg gac ggg gtc cgc gag aag agc gac cca cac atc aaa 241
106  Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys
107          65          70          75
108  cta caa ctt caa gca gaa gag aga ggg gtt gtg tct atc aaa gga gtg 289
109  Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val
110          80          85          90
111  tgt gca aac cgt tac ctt gct atg aaa gaa gat gga aga tta cta gct 337
112  Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala
113          95          100          105
114  tct aaa tgt gtt aca gac gag tgt ttc ttt ttt gaa cga ttg gag tct 385
115  Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser
116          110          115          120          125
117  aat aac tac aat act tac cgg tca agg aaa tac acc agt tgg tat gtg 433
118  Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val
119          130          135          140
120  gca ctg aaa cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct 481
121  Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro
122          145          150          155
123  ggg cag aaa gct ata ctt ttt ctt cca atg tct gct aag agc gaa cag 529
124  Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln
125          160          165          170
126  aaa ctc atc tct gaa gag gat ctg tga 556
127  Lys Leu Ile Ser Glu Glu Asp Leu
128          175          180
129 <210> SEQ ID NO 4
130 <211> LENGTH: 181
131 <212> TYPE: PRT
132 <213> ORGANISM: chimeric sequence
133 <400> SEQUENCE: 4
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135          1          5          10          15
136  Ala Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
137          20          25          30
138  Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
139          35          40          45
140  Tyr Cys Lys Asn Gly Gly Phe Leu Arg Ile His Pro Asp Gly Arg
141          50          55          60
142  Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
143          65          70          75          80
144  Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn

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145              85              90              95
146    Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
147              100              105              110
148    Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
149              115              120              125
150    Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
151              130              135              140
152    Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
153    145              150              155              160
154    Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Glu Gln Lys Leu Ile
155              165              170              175
156    Ser Glu Glu Asp Leu
157              180
158    <210> SEQ ID NO 5
159    <211> LENGTH: 146
160    <212> TYPE: PRT
161    <213> ORGANISM: Bos taurus
162    <400> SEQUENCE: 5
163    Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
164    1              5              10              15
165    Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
166              20              25              30
167    Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
168              35              40              45
169    Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
170    50              55              60
171    Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
172    65              70              75              80
173    Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
174              85              90              95
175    Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
176              100              105              110
177    Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
178              115              120              125
179    Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
180    130              135              140
181    Lys Ser
182    145
183    <210> SEQ ID NO 6
184    <211> LENGTH: 146
185    <212> TYPE: PRT
186    <213> ORGANISM: Homo sapiens
187    <400> SEQUENCE: 6
188    Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
189    1              5              10              15
190    Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
191              20              25              30
192    Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
193    35              40              45
194    Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser

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195          50          55          60
196 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
197    65          70          75          80
198 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
199          85          90          95
200 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
201          100          105          110
202 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
203          115          120          125
204 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
205          130          135          140
206 Lys Ser
207    145
208 <210> SEQ ID NO 7
209 <211> LENGTH: 140
210 <212> TYPE: PRT
211 <213> ORGANISM: Bos taurus
212 <400> SEQUENCE: 7
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214    1          5          10          15
215 Ser Asn Gly Gly Tyr Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp
216          20          25          30
217 Gly Thr Lys Asp Arg Ser Asp Gly His Ile Gln Leu Phe Leu Cys Ala
218          35          40          45
219 Glu Ser Ile Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Phe
220          50          55          60
221 Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asp
222          65          70          75          80
223 Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr
224          85          90          95
225 Tyr Ile Ser Lys Lys His Ala Glu Lys His Trp Phe Val Gly Leu Lys
226          100          105          110
227 Lys Asn Gly Arg Ser Lys Leu Glu Pro Arg Thr His Phe Gly Gln Lys
228          115          120          125
229 Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
230          130          135          140
231 <210> SEQ ID NO 8
232 <211> LENGTH: 140
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
235 <400> SEQUENCE: 8
236 Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys
237    1          5          10          15
238 Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Tyr Asp
239          20          25          30
240 Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala
241          35          40          45
242 Glu Ser Tyr Gly Glu Tyr Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr
243          50          55          60
244 Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn

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Line ? Error/Warning

Original Text

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